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N-TERMINAL

P26h	MK	LN	FS	XL	RA	LV	TG	AG	KG	IG	IG	XD	TA	KA	L
Adipsin	--	--	--	G-	--	--	--	--	--	--	--	R-	-V	--	--

NCS FRAGMENT

P26h	XA	TE	KA	LG	XI	GP	VX	XL	VN	NA	AL	XX	XQ
Adipsin	D-	--	--	--	G-	--	-D	L-	--	--	--	VM	I-

CNBr fragment

P26h	LY	PY	KX	RV	N
Adipsin	-G	-H	-I	--	--

FILE-1

1 2 3 4 5 6 7 8 9 10 11 12

1081 -

Cyclophilin

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FIG. 2

GTCCCTGGAGGTTGGCTGTAGGATTCAGGTGGCTTGCTCAGGCTGGG 47
 ATCAAGGACACAGTGAGCAGATCAACCTTAACCTCAGCCCTCCC 92
 CTCGCCACAGGAGGACACTGGTGTCTCAGCAGCATG AAG CTG AAT 135
 M K L N 4

TTC ACT GGT CTC AGG GCT CTG GTG ACC GGG GCA GGG AGA GGG 177
 F T G L R A L V T G A G R G 18

ATT GGG CGA GGC ACT GCG AAA GCC CTG CAT GCC TCA GGA GCC 219
 I G R G T A K A L H A S G A 32

AAA GTG GTG GCC GTG TCA CTC ATC AAC GAA GAC CTG GTC AGC 261
 K V V A V S L I N E D L V S 46

CTG GCC AAA GAG TGT CCG GGC ATA GAG CCT GTG TGT GTG GAC 303
 L A K E C P G I E P V C V D 60

CTG GGT GAC TGG GAG GCC ACA GAG AAG GCA CTG GGC CGT ATT 345
 L G D W E A T E K A L G R I 74

GGC CCC GTG GAC CTG GTG AAC AAT GCG GCG GTG GCG CTA 387
 G P V D L L V N N A A V A L 88

FEF-3A

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GTG CAG CCT TTC ATA CAG TCT ACC AAG GAG GTC TTT GAC AGG 429
 V Q P F I Q S T K E V F D R 102

 TCC TTC AAT GTG AAT GTG CGC TCT GTG CTG CAA GTG TCC CAG 471
 S F N V N V R S V L Q V S Q 116

 ATG GTA GCC AAG GGC ATG ATT AAC CGT GGA GTG GCA GGA TCC 513
 M V A K G M I N R G V A G S 130

 ATT GTC AAC ATC TCC AGC ATG GTG GCC TAT GTC ACC TTC CCT 555
 I V N I S S M V A Y V T F P 144

 GGT CTG GCC ACG TAC AGC TCC ACC AAG GGT GCT ATA ACC ATG 597
 G L A T Y S S T K G A I T M 158

 CTG ACC AAA GCC ATG GCC ATG GAG CTG GGA CCA TAC AAG ATC 639
 L T K A M A M E L G P Y K I 172

 CGG GTG AAC TCT GTA AAC CCT ACC GTG GTG CTG ACT GAC ATG 681
 R V N S V N P T V V L T D M 186

 GGC AAG AAA GTC TCT GCA GAC CCG GAA TTT GCC AAG AAG CTC 723
 G K K V S A D P E F A K K L 200

 115-3B

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AAG GAG CGC CAC CCA CTG AGG AAG TTC GCA GAG GTG GAG GAC 765
 K E R H P L R K F A E V E D 214

GTG GTC AAC AGC ATC CTC TTC CTG CTC AGC GAC AGC AGC GCC 807

V V N S I L F L L S D S S A 228

TCT ACC AGC GGC TCT GGC ATC CTG GTG GAC GCT GGT TAC CTG 849
 S T S G S G I L V D A G Y L 242

GCC TCC TAG ACGGCCCAGGTGCAGGGGACTCCTGGAGACTTCC 892
 A S Amber 244

CTGGCCTCACCCCTTACATCAAGACCCCGCCCTTCAACCCCAATAAT 941
 TTGTTCGAATCCTGTAGAGCCCCACCCACACACATCCATCCCCAACT 990
 TTAGACTCCGGGATCCCGCCATTCCATACCAAGCTATGCTGAGATAATT 1038
 TGATTAAATAAGTATCCCAACCACAAAAAATAAAAAA 1081

— FIG. 3 —

P26h	MK LN FT GL RA LV TG AG RG IG RG TA KA LH AS GA KV VA VS LI NE DL VS LA KE	50
Adipsin	- - - S - - - - - D - V - - - - - T RT - S - - - - -	50
C.Reductase	- Q M - S - - - - K - - - D - V - - - V - - - R - - - T RT - G - - - - S Q - 50	
P26h	CP GI EP VC VD LG DWEA TE KA LG RI GP VD LL VN NA AV AL VQ PF IQ ST KE VF	100
Adipsin	- - - - - D - - - - G - - - - - L VI M - - - LE V - - - A - 100	
C.Reductase	- - - - - R - - - - GV - - - - - M - - - - LD T - - - - 100	
P26h	DR SF NV NV RS VL QV SQ MV AK GMIN RG VA GS IV NI SS MVAY VT FP GL AT YS	150
Adipsin	- - - S - L - - - F - - - - R D - - - - P - - - - V - - - - H - - - - N - I - - - 150	
C.Reductase	- - - - - L - - - F - - - - I - - R S - E - - - P - - - - V - - - - SH - - - Y - - - - A - - 150	

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FILE - 4A

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P26h	ST KG AI TMLT KA MAMELG PY KI RV NS VN PT VV LT DMGK KV SA DP EF AK KL	200
Adipsin	-- -- -M -- -- -- -- -H -- -- -- -- -- -- -- -- -- -- -R --	200
C.Reductase	-- -- -M -- -- -S -- -- -H -- -- -- -- -- A- -R S- TS -- -L -R --	200
P26h	KE RH PL RK FA EV ED VV NS IL FL LS DS SA ST SG SG IL VD AG YL AS	244
Adipsin	-- -- -- -- -- -- -- -- -- -- -R -- -- -- -- G- -- -- -- -- --	244
C.Reductase	-- -- -M -- -- -- -- -- -R -- -- -- -- -S -F -- -- -- --	244

FILE - 4B

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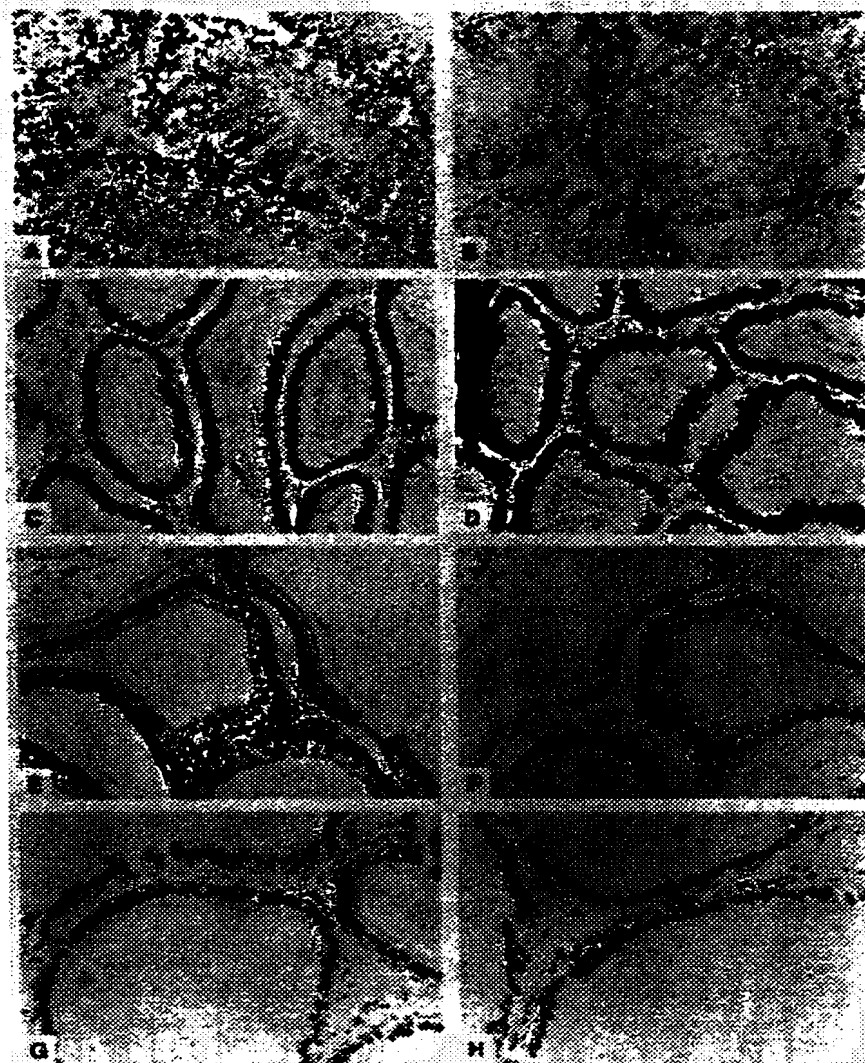


FIG. 5

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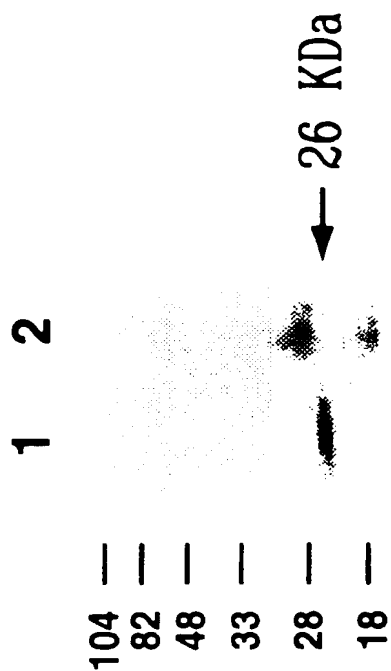


Fig. 6B

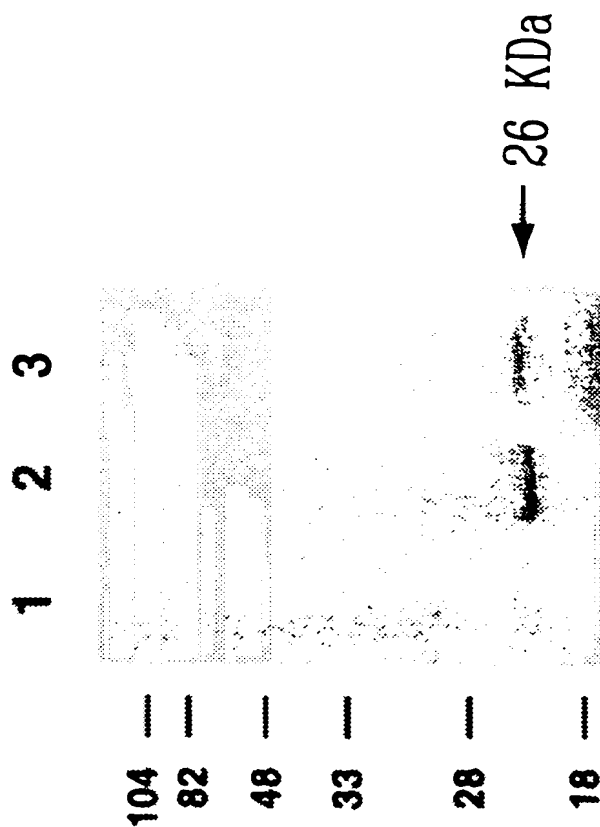


Fig. 6A

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Epididymis

M

Testis

Caput

Corpus

Cauda



← 913 bp

7

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10		20		30		40		50		60		70		80	
MKLNFTGLRALVTGAGRGIGRGTAHALHASGAKVAVSLINEDLVSLAKECPGIEPVCVDLGDWEATEKALGRIGPVDLL															
.
MELFLAGRRVLVTGAGKGIGRGTVQALHATGARVVAVSRTQADLDSLVRCECPGIEPVCVDLGDWEATERALGSVGPVDLL															
10		20		30		40		50		60		70		80	

90		100		110		120		130		140		150		160	
VNNAAVALLVQPFIQSTKEVDFDRSFNVNVRSVLQVSQMVAKGMINRGVAGSIVNISSMVAVTFPGLATYSSTKGAIITMLT															
.
VNNAAVALLQPFLEVTKAEAFDRSFEVNLRAVIQVSQIVARGLIARGVPGAIENVSSQCSQRAVTNHSVYCSTKGALDMLT															
90		100		110		120		130		140		150		160	

FILE - BA

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170		180		190		200		210		220		230		240
KAMAMELG	PYKIRV	NSVNPT	VLTDMG	KKVSAD	PEFAK	TLFERH	PLRFAE	VEDVNS	ILFLSD	SSASTG	SGILVD	AG		
• • • • •	• • • • •	• • • • •	• • • • •	• • • • •	• • • • •	• • • • •	• • • • •	• • • • •	• • • • •	• • • • •	• • • • •	• • • • •	• • • • •	• • • • •
KVMALEL	GPHKIR	VNAVNP	TVMGQ	ATWSDP	HKAKT	MLNRIF	LGKFAE	VEHVNA	ILFLSD	RSRSGM	TTGSTL	PVERG		
170		180		190		200		210		220		230		240

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FIG. 88